

Amendment and Response

Serial No.: 09/866,307

Confirmation No.: 4705

Filed: May 25, 2001

For: DNA MOLECULES AND PROTEIN DISPLAYING IMPROVED TRIAZINE COMPOUND DEGRADING ABILITY

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Please replace the paragraph beginning at page 7, line 21, with the following rewritten paragraph. Per 37 C.F.R. §1.121, this paragraph is also shown in Appendix A with notations to indicate the changes made.

Figs. 1A-C. Nucleotide sequence alignment of wild type *atzA* (bottom sequence) from *Pseudomonas sp.* strain ADP and clone (A7) (SEQ ID NO:1 and SEQ ID NO:3). The boxed sequences indicate areas of nonidentity between the two nucleotide sequences.

Please replace the paragraph beginning at page 7, line 24, with the following rewritten paragraph. Per 37 C.F.R. §1.121, this paragraph is also shown in Appendix A with notations to indicate the changes made.

Figs. 2A-C. Nucleotide sequence alignment of wild type *atzA* (bottom sequence) from *Pseudomonas sp.* strain ADP and clone (T7) (SEQ ID NO: 1 and SEQ ID NO:4). The boxed sequences indicate areas of nonidentity between the two nucleotide sequences.

Please replace the paragraph beginning at page 8, line 1, with the following rewritten paragraph. Per 37 C.F.R. §1.121, this paragraph is also shown in Appendix A with notations to indicate the changes made.

Figs. 5A-D. Nucleotide sequence alignment of wild type *atzA* (SEQ ID NO:1, bottom sequence) from *Pseudomonas sp.* strain ADP and clone (A11). Fig. 5(a) provides the sequence from nucleic acids 11-543 (SEQ ID NO:7), Fig. 5(b) provides the sequence from nucleic acids 454-901 (SEQ ID NO:8), Fig. 5(c) provides the sequence from 1458-1851 (SEQ ID NO:9; N in this sequence indicates that this nucleotide has not been verified) and Fig. 5(d) provides the sequence from nucleic acids 1125-1482 (SEQ ID NO:10) of clone A11. The boxed sequences indicate areas of nonidentity between the two nucleotide sequences. The "N" in these sequences refer to nucleic acids that are being verified. The four "C" nucleotides depicted above the top sequence in 5(a) and the eleven "G" nucleotides depicted above the top sequence in 5(b) indicate the correct nucleotide sequence of the top sequence.

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Please replace the paragraph beginning at page 8, line 12, with the following rewritten paragraph. Per 37 C.F.R. §1.121, this paragraph is also shown in Appendix A with notations to indicate the changes made.

c5 **Figs. 7A-B.** are histograms illustrating the TERBUTHYLAZINE degradative ability of two homologs of this invention (T7= sample 3 and A7 = sample 4). Fig. 7(a) illustrates the % of TERBUTHYLAZINE remaining after exposure to AtzA or a homolog. Fig. 7(b) illustrates the relative amount of hydroxyterbuthylazine as a measure of TERBUTHYLAZINE degradation.

Please replace the paragraph beginning at page 8, line 17, with the following rewritten paragraph. Per 37 C.F.R. §1.121, this paragraph is also shown in Appendix A with notations to indicate the changes made.

cb **Figs. 8A-B.** are histograms illustrating the terbuthylazine degradative ability of three homologs A7, All, and T7. Figure 8(a) provides the % of TERBUTHYLAZINE remaining after a 15 minute exposure to the homolog in the presence or absence of the metals and additives of Samples 1-10. Figure 8(b) provides the relative amount of hydroxterbuthylazine in the presence or absence of the metals and compounds of Samples 1-10.

Please replace the paragraph beginning at page 8, line 23, with the following rewritten paragraph. Per 37 C.F.R. §1.121, this paragraph is also shown in Appendix A with notations to indicate the changes made.

c7 **Fig. 9.** is a comparison of PCR amplified fragments using two primers of the atrazine hydrochlorase gene from 6 different types of bacteria; *Pseudomonas* sp. Strain ADP (SEQ ID NO:16); *Ralstonia* strain M91-3 (SEQ ID NO:13); *Clavibacter* (*Clav.*) (SEQ ID NO:16); *Agrobacterium* strain J14(a) (SEQ ID NO:14); ND (an organism with no genus assigned) strain 38/38 (SEQ ID NO:15); and *Alcaligenese* strain SG1 (SEQ ID NO:12).